SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Role, Lorna W.

    (ii) TITLE OF INVENTION: SPLICE VARIANTS OF THE HEREGULIN GENE,
nARIA,
                       AND USES THEREOF

    (iii) NUMBER OF SEQUENCES: 4

    (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Cooper & Dunham LLP
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        (C) CITY: New York
        (D) STATE: New York
        (E) COUNTRY: U.S.A.
        (F) ZIP: 10036

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER:
        (B) FILING DATE:
        (C) CLASSIFICATION:

    (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: White, John P.
        (B) REGISTRATION NUMBER: 28,678
        (C) REFERENCE/DOCKET NUMBER: 46839-A

    (ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: 212-278-0400
        (B) TELEFAX: 212-391-0526

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3212 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGATGCTGC TGCTACTGTC ACTTCTGCCG CTGCCGCTGT TGTTACAGAT TTTGCTTTTG
           60

CTCCTTCTAC CGCATGACAA TTGTTTTCCT CGCCTAAGCA GATACCAGCC TCAGATGCTC
           120

AAGGTGAGAG TCTTGCCTTT CGCTCTGGGC TATTGGTTCA CTTAATCCGG TCAATTTGTT
           180

CGCTGCTCGT GGTTGTCTTT CTCCCCGCCC TCCTTCCCCC TGTTTTGTTT TGTTTCGCTT
           240

GCTTTCGGGG GGACGCTCCT TCCCTCAGTC AGAAGAGCTG GAATTGCTTG AGAGGCGTAT
           300

AAGGAATTAT AAAAGTGGCC AGGAAACACG AGCGCAGTGA CTGCAGAGCT GCCCTTGGCT
           360

TCGGCAAGGC AGCGTGAGCG GCAGAGGGCT CGGGCAGGGG GCGGGGGGTC TCCTTTTTCC
           420

CGTGCGTTCC TCTTCTCCCA GTTCGGATGA TGTTGCTGTT TCGGACCTCT CGCTGACTCC
           480

TGCCCTGTGA TTTTTGCTGA GCGCTGTGAC TGTTACTCCG TCTCTTTCTG TCTGTGTTTC
           540

ACAGTAATGG ACTGTGATAG AGTTAAGGCC TTTTGGAGGT GAGCTGTGTC ACAGCTGATG
           600

CTTAAACATG TCTGAAGTAG GCACCGAGAC TTTCCCCAGC CCCTCGGCTC AGCTGAGCCC
           660

TGATGCATCC CTTGGCGGGC TCCCGGCTGA GGAGAACATG CCGGGGCCCC ACAGAGAGGA
           720

CAGCAGGGTC CCAGGTGTGG CAGGCCTGGC CTCGACCTGC TGCGTGTGCC TGGAAGCAGA
           780

GCGACTGAAG GGCTGCCTCA ACTCTGAGAA GATCTGCATC GCCCCTATCC TGGCTTGCCT
           840

GCTCAGCCTC TGCCTCTGCA TTGCTGGCCT CAAGTGGGTC TTTGTGGACA AGATTTTTGA
           900

GTATGACTCT CCTACACACC TTGACCCTGG GAGGATAGGA CAAGACCCAA GGAGCACTGT
           960

GGATCCTACA GCTCTGTCTG CCTGGGTGCC TTCGGAGGTG TATGCCTCAC CCTTCCCCAT

1020

ACCTAGCCTT GAGAGCAAGG CTGAAGTGAC AGTGCAAACT GACAGCTCGC TCGTGCCCTC
1080

CAGGCCCTTC CTTCAGCCTT CTCTCTACAA CCGCATCCTA GATGTCGGGT TGTGGTCCTC
1140

TGCCACACCG TCACTGTCAC CATCCTCCCT GGAGCCTACC ACGGCATCTC AGGCACAAGC
1200

AACAGAAACC AATCTCCAAA CTGCTCCAAA ACTTTCCACT TCTACATCTA CAACTGGGAC
1260

AAGTCATCTC ACAAAATGTG ACATAAAGCA GAAAGCCTTC TGTGTAAATG GGGGAGAGTG
1320

CTACATGGTT AAAGACCTCC CAAACCCTCC ACGATACCTA TGCAGGTGCC CAAATGAATT
1380

TACTGGTGAT CGCTGCCAAA ACTACGTAAT GGCCAGCTTC TACAAGCATC TTGGGATTGA
1440

ATTTATGGAA GCTGAGGAAC TGTACCAGAA ACGGGTGCTG ACCATAACTG GCATTTGCAT
1500

TGCTCTTCTA GTAGTTGGCA TCATGTGTGT GGTGGCCTAC TGCAAAACCA AGAAGCAGAG
1560

GAAAAAGTTG CATGACCGCC TTCGGCAGAG CCTTCGCTCA GAGAGGAACA ACGTTATGAA
1620

CATGGCAAAT GGGCCACACC ACCCCAACCC ACCACCAGAC AATGTCCAGC TGGTGAATCA
1680

GTACGTTTCA AAAACATAA TCTCCAGTGA ACGTGTCGTT GAGCGAGAAA CCGAGACCTC
1740

GTTTTCCACA AGCCACTACA CCTCAACAAC TCATCACTCC ATGACAGTCA CCCAGACGCC
1800

TAGCCACAGC TGGAGTAATG GCCATACCGA AAGCATTCTC TCCGAAAGCC ACTCCGTGCT
1860

CGTCAGCTCC TCAGTGGAGA ATAGCAGGCA CACCAGCCCA ACAGGGCCAC GAGGCCGCCT
1920

CAATGGCATT GGTGGGCCAA GGGAAGGCAA CAGCTTCCTC CGGCATGCAA GAGAGACCCC
1980

TGACTCCTAC CGAGACTCTC CTCACAGTGA AAGGTATGTC TCAGCTATGA CCACACCAGC
2040

TCGCATGTCA CCCGTTGATT TCCACACTCC AACTTCTCCC AAGTCCCCTC CATCTGAAAT
2100

GTCACCACCA GTTTCCAGCT TGACCATCTC CATCCCTTCG GTGGCGGTGA GTCCCTTTAT
2160

GGACGAGGAG AGACCGCTGC TGTTGGTGAC CCCACCACGG CTGCGTGAGA AGTACGACAA
2220

CCACCTTCAG CAATTCAACT CCTTCCACAA CAATCCCACC CATGAGAGCA ACAGTCTGCC
2280

ACCCAGTCCT CTGAGGATAG TGGAGGATGA AGAGTATGAG ACCACGCAGG AGTACGAACC
2340

AGCACAGGAG CCTCCAAAGA AACTCACCAA CAGCCGGAGG GTGAAAAGAA CAAAGCCCAA
2400

TGGCCATATT TCCAGCAGGG TAGAAGTGGA CTCCGACACA AGCTCTCAGA GCACTAGCTC
2460

TGAGAGCGAA ACAGAAGATG AAAGAATAGG TGAGGATACA CCATTTCTTA GCATACAAAA
2520

TCCCATGGCA ACCAGTCTGG AGCCAGCCGC TGCATATCGG CTGGCTGAGA ACAGGACTAA
2580

CCCGGCAAAT CGCTTCTCCA CACCAGAAGA GTTGCAAGCA AGGTTGTCCA GTGTAATAGC
2640

TAACCAAGAC CCTATTGCTG TATAAGACAT AAACAAAACA CATAGATTCA CATGTAAAAC
2700

TTTATTTTAT ATAATGAAGT ATTCCACCTT TAAATTAAAC AATTTATTTT ATTTTAGCAA
2760

TTCCGCTGAT AGAAAACAAG AGTGGAAAAA GAAACTTTTA TAAATTAAGT ATACGTATGT
2820

ACAAATGTGT TATGTGCCAT ATGTAGCAAT TTTTTACAGT ATTTCCAAAA TGGGGAAAGA
2880

TATCAATGGT GCCTTTATGT TATGTTATGT TGAGAGCAAG TTTTGTACAG CTACAATGAT
2940

TGCTGTCCCG TAGTATTTTG CAAAACCTTC TAGCCCTCAG TTGTTCTGGC TTTTTTGTGC
3000

ATTGCATTAT AATGACTGGA TGTATGATTT GCAAGAATTG CAGAAGTCCC CATTTGCTTG
3060

TTGTGGAATC CCCAGATCAA AAAGCCCTGT TATGGCACTC ACACCTATC CACTTCACCA

3120

GGAAAAAAAA AAAATCAAAA AAAAAAAAAA AAAAAAAAGA AAAGAAGAG AAAAAGAAA
  3180

AGAAAAAGAA AAAAAAAGCT GAAAAAATAA AA
  3212

(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1070 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg
        Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr
        1   5   10   15

Xaa
        Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala
                    20   25   30

Leu
        Ala Asp Thr Ser Leu Arg Cys Ser Arg Xaa Glu Ser Cys Leu Ser
                    35   40   45

Gly
        Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg
                    50   55   60

Leu
        Cys Leu Ser Pro Arg Pro Pro Ser Pro Cys Phe Val Leu Phe Arg
        65   70   75   80

Leu
        Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu
                    85   90   95

Gln   Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala
                    100   105   110

Arg   Xaa Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly
                    115   120   125

Ser   Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser
                130   135   140

Pro   Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr
160   145   150   155

Ser   Ala Leu Xaa Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu
                    165   170   175

Gly   Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe
                    180   185   190

Thr   Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly
                    195   200   205

Leu   Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser
                    210   215   220

Asp   Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu
240   225   230   235

Cys   Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val
                    245   250   255

Cys   Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile

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                      260                   265                        270

        Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile
Ala
                  275                   280                   285

        Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser
Pro
                  290                   295                   300

        Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr
Val
                  305                   310                   315
320

        Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala
Ser
                      325                   330                   335

        Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val
Gln
                      340                   345                   350

        Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser
Leu
                      355                   360                   365

        Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro
Ser
                  370                   375                   380

        Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Gln Ala Gln
Ala
                  385                   390                   395
400

        Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr
Ser
                      405                   410                   415

        Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys
Ala
                      420                   425                   430
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```
        Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro
Asn
            435                 440                 445

        Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp
Arg
            450                 455                 460

        Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile
Glu
        465                 470                 475
480
        Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile
Thr
                        485                 490                 495

        Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val
Ala
                500                 505                 510

        Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu
Arg
                515                 520                 525

        Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn
Gly
            530                 535                 540

        Pro His His Pro Asn Pro Pro Pro Asp Asn Val Gln Leu Val Asn
Gln
        545                 550                 555
560
        Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg
Glu
                        565                 570                 575

        Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His
His
                580                 585                 590

        Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly
His
```

```
                    595                       600                       605

        Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser
Ser
                    610                       615                       620

        Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg
Leu
                    625                       630                       635
640
        Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His
Ala
                                645                       650                       655

        Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg
Tyr
                                660                       665                       670

        Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe
His
                                675                       680                       685

        Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro
Val
                    690                       695                       700

        Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe
Met
                    705                       710                       715
720
        Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg
Glu
                                725                       730                       735

        Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn
Pro
                                740                       745                       750

        Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val
Glu
                                755                       760                       765
```

```
Pro     Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu
            770             775             780

Asn     Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro
800         785             790             795

Gln     Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser
                        805             810             815

Asp     Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu
                        820             825             830

Pro     Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu
                    835             840             845

Arg     Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn
                850             855             860

Ala     Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile
880         865             870             875

Phe     Asn Gln Asp Pro Ile Ala Val Xaa Asp Ile Asn Lys Thr His Arg
                        885             890             895

Leu     Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys
                    900             905             910

Trp     Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu
                    915             920             925

Tyr     Lys Lys Lys Leu Leu Xaa Ile Lys Tyr Thr Tyr Val Gln Met Cys
```

```
                 930                      935                      940

      Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys
Asp
960   945                      950                      955

      Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys
Thr
                     965                      970                      975

      Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser
Pro
                     980                      985                      990

      Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met
Tyr
                     995                      1000                     1005

      Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile
Pro
                 1010                     1015                     1020

      Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His
Gln
1040  1025                     1030                     1035

      Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Lys Arg Lys Glu
Arg
                     1045                     1050                     1055

      Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser Xaa Lys Asn Lys
                     1060                     1065                     1070
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1351 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CGGCCTGTAA GATGCTGTAT CATTTGGTTG GGGGGGCCTC TGCGTGGTAA TGGACCGTGA
    60

GAGCGGCCAG GCCTTCTTCT GGAGGTGAGC CGATGGAGAT TTATTCCCCA GACATGTCTG
   120

AGGTCGCCGC CGAGAGGTCC TCCAGCCCCT CCACTCAGCT GAGTGCAGAC CCATCTCTTG
   180

ATGGGCTTCC GGCAGCAGAA GACATGCCAG AGCCCCAGAC TGAAGATGGG AGAACCCCTG
   240

GACTCGTGGG CCTGGCCGTG CCCTGCTGTG CGTGCCTAGA AGCTGAGCGC CTGAGAGGTT
   300

GCCTCAACTC AGAGAAAATC TGCATTGTCC CCATCCTGGC TTGCCTGGTC AGCCTCTGCC
   360

TCTGCATCGC CGGCCTCAAG TGGGTATTTG TGGACAAGAT CTTTGAATAT GACTCTCCTA
   420

CTCACCTTGA CCCTGGGGGG TTAGGCCAGG ACCCTATTAT TTCTCTGGAC GCAACTGCTG
   480

CCTCAGCTGT GTGGGTGTCG TCTGAGGCAT ACACTTCACC TGTCTCTAGG GCTCAATCTG
   540

AAAGTGAGGT TCAAGTTACA GTGCAAGGTG ACAAGGCTGT TGTCTCCTTT GAACCATCAG
   600

CGGCACCGAC ACCGAAGAAT CGTATTTTTG CCTTTTCTTT CTTGCCGTCC ACTGCGCCAT
   660

CCTTCCCTTC ACCCACCCGG AACCCTGAGG TGAGAACGCC CAAGTCAGCA ACTCAGCCAC
   720

AAACAACAGA AACTAATCTC CAAACTGCTC CTAAACTTTC TACATCTACA TCCACCACTG
   780

GGACAAGCCA TCTTGTAAAA TGTGCGGAGA AGGAGAAAAC TTTCTGTGTG AATGGAGGGG
   840

AGTGCTTCAT GGTGAAAGAC CTTTCAAACC CCTCGAGATA CTTGTGCAAA GGCGGAGGAG
   900

CTGTACCAGA AGAGAGTGCT GACCATAACC GGCATCTGCA TCGCCCTCCT TGTGGTCGGC
   960

ATCATGTGTG TGGTGGCCTA CTGCAAAACC AAGAAACAGC GGAAAAAGCT GCATGACCGT
  1020
```

CTTCGGCAGA GCCTTCGGTC TGAACGAAAC AATACGATGA ACATTGCCAA TGGGCCTCAC
  1080

CATCCTAACC CACCCCCCGA GAATGTCCAG CTGGTGAATC AATACGTATC TAAAAACGTC
  1140

ATCTCCAGTG AGCATATTGT TGAGAGAGAA GCAGAGACAT CCTTTTCCAC CAGTCACTAT
  1200

ACTTCCACAG CCCATCACTC CACTACTGTC ACCCAGACTC CTAGCCACAG CTGGAGCAAC
  1260

GGACACACTG AAAGCATCCT TTCCGAAAGC CACTCTGTAA TCGTGATGTC ATCCGTAGAA
  1320

AACAGTAGGC ACAGCAGCCC AACTGGGGCC G
  1351

(2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 449 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

        Ala Cys Lys Met Leu Tyr His Leu Val Gly Gly Ala Ser Ala Trp
Xaa
        1   5   10   15

        Trp Thr Val Arg Ala Ala Arg Pro Ser Ser Gly Gly Glu Pro Met
Glu
                    20   25   30

        Ile Tyr Ser Pro Asp Met Ser Glu Val Ala Ala Glu Arg Ser Ser
Ser
                    35   40   45

        Pro Ser Thr Gln Leu Ser Ala Asp Pro Ser Leu Asp Gly Leu Pro
Ala
            50   55   60

```
         Ala Glu Asp Met Pro Glu Pro Gln Thr Glu Asp Gly Arg Thr Pro
Gly
         65                  70                  75                  80

         Leu Val Gly Leu Ala Val Pro Cys Cys Ala Cys Leu Glu Ala Glu
Arg
                         85                  90                  95

         Leu Arg Gly Cys Leu Asn Ser Glu Lys Ile Cys Ile Val Pro Ile
Leu
                         100                 105                 110

         Ala Cys Leu Val Ser Leu Cys Leu Cys Ile Ala Gly Leu Lys Trp
Val
                         115                 120                 125

         Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro Thr His Leu Asp
Pro
                         130                 135                 140

         Gly Gly Leu Gly Gln Asp Pro Ile Ile Ser Leu Asp Ala Thr Ala
Ala
         145                 150                 155
160

         Ser Ala Val Trp Val Ser Ser Glu Ala Tyr Thr Ser Pro Val Ser
Arg
                         165                 170                 175

         Ala Gln Ser Glu Ser Glu Val Gln Val Thr Val Gln Gly Asp Lys
Ala
                         180                 185                 190

         Val Val Ser Phe Glu Pro Ser Ala Ala Pro Thr Pro Lys Asn Arg
Ile
                         195                 200                 205

         Phe Ala Phe Ser Phe Leu Pro Ser Thr Ala Pro Ser Phe Pro Ser
Pro
                         210                 215                 220

         Thr Arg Asn Pro Glu Val Arg Thr Pro Lys Ser Ala Thr Gln Pro
Gln
```

```
              225                    230                         235
240
        Thr Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser
Thr
                             245                    250                    255

        Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu
Lys
                         260                    265                    270

        Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu
Ser
                     275                    280                    285

        Asn Pro Ser Arg Tyr Leu Cys Lys Gly Gly Gly Ala Val Pro Glu
Glu
                 290                    295                    300

        Ser Ala Asp His Asn Arg His Leu His Arg Pro Pro Cys Gly Arg
His
        305                    310                    315
320

        His Val Cys Gly Gly Leu Leu Gln Asn Gln Glu Thr Ala Glu Lys
Ala
                     325                    330                    335

        Ala Xaa Pro Ser Ser Ala Glu Pro Ser Val Xaa Thr Lys Gln Tyr
Asp
                 340                    345                    350

        Glu His Cys Gln Trp Ala Ser Pro Ser Xaa Pro Thr Pro Arg Glu
Cys
                 355                    360                    365

        Pro Ala Gly Glu Ser Ile Arg Ile Xaa Lys Arg His Leu Gln Xaa
Ala
             370                    375                    380

        Tyr Cys Xaa Glu Arg Ser Arg Asp Ile Leu Phe His Gln Ser Leu
Tyr
        385                    390                    395
400
```

```
       Phe His Ser Pro Ser Leu His Tyr Cys His Pro Asp Ser Xaa Pro
Gln                    405                 410                 415

       Leu Glu Gln Arg Thr His Xaa Lys His Pro Phe Arg Lys Pro Leu
Cys                    420                 425                 430

       Asn Arg Asp Val Ile Arg Arg Lys Gln Xaa Ala Gln Gln Pro Asn
Trp                    435                 440                 445

Gly
```